

Taxonomic Identification
J-15-34/35

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Submitter: [REDACTED]

Identification of Recipient used in J-15-34/35

Production strain:

The production strains, [REDACTED], are derived from the parental strain with an internal designation of [REDACTED]. The parental strain [REDACTED] which was identified as *Saccharomyces cerevisiae*.

Taxonomy of the recipient:

This strain, [REDACTED] At that time, and subsequently for [REDACTED] and the current cases, the submitter was shown to be identified as [REDACTED], who used both [REDACTED]. However, in the earlier cases, as well as for the recipient of this case, a relevant comparator was not included in the MIDI analysis. A strain, called either *S. boulardii* or *S. cerevisiae* var. *boulardii* was not included in the recipient analysis, even though it may be possible, but very difficult, to differentiate this alternative from *S. cerevisiae* (Malgoire et al. 2005). This comparison taxon was included in the tables for the modified production strains, and, even though they are derived from [REDACTED], the results were different once *S. boulardii* (*sic*) was included. In those cases, the strains could not be differentiated from either *S. cerevisiae* or *S. boulardii*. Using public sequences for 34 strains, 7 "*boulardii*" and 27 *cerevisiae*, alignments using Lasergene Megalign and MegalignPro (DNASTar, Inc.) were attempted using the data supplied to us in a supplement dated 9/4/2015. The sequence for [REDACTED] was too divergent to align using Megalign but was aligned using MegalignPro. The provided 28S sequences could only be compared with four strains of *S. cerevisiae*, because the sequences supplied only overlapped with the portion of the 28S gene for those strains. None of the public sequences for "*boulardii*" contained sequences that could be compared with the ones for [REDACTED] or its derivatives.

Conclusion regarding the recipient:

The identification of the subject microorganisms cannot definitively be assigned to *S. cerevisiae*, although if regarded as a variety of this species, "*boulardii*" strains would fall within that larger taxon. Given the unsettled nature of the systematics relevant to *S. boulardii*, it is not now possible to determine which *Saccharomyces* species the recipient and derivatives belong to.

Donors:

[REDACTED]

Reference

Malgoire, J., S.Bertout, F.Renaud, J. Bastide and M. Mallié. 2005. Typing of *Saccharomyces cerevisiae* clinical strains by using microsatellite sequence polymorphism. J. Clin. Microbiol. **43**:1133-1137